

FIG. 13A

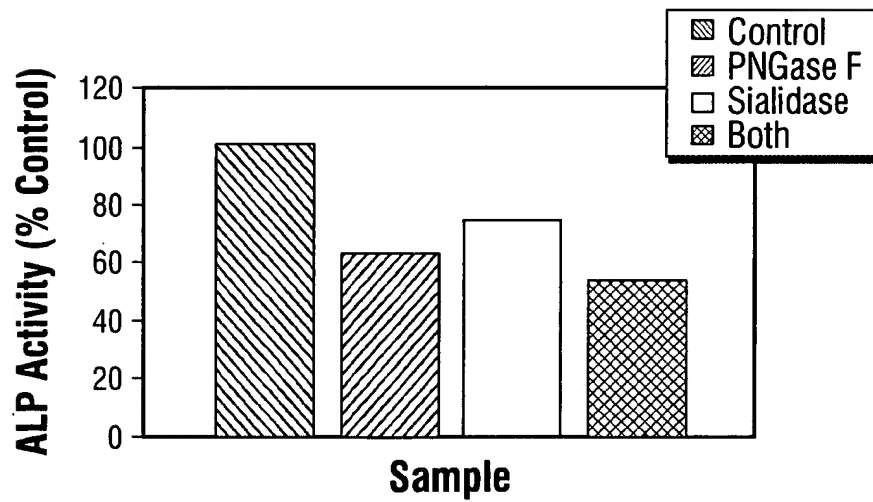


FIG. 13B



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	SEQ. ID NO:	Best Database Match	SEQ. ID NO:
1					
2	fx 49 (1579)	XLAAAGYDVEK	1	ALAAAGYDVEK	2
3	fx 67 (1346)	SLEKVCADLIR	3	SLEKVCADLIR	3
4	fx 65 ()	(V)VCGMLGFPSEAPV	4	VVCGMLGFPGEKRV	5
5	N terminal seq	STGVLLPLQNNELGP	6	STGVLLPLQNNELPG	6
	fx 72 (3925)	STGVLLPLQNNELPGAIEYQY	7	STGVLLPLQNNELPGAIEYQY	7
	fx 74 (3409)	STGVLLPLQ	8	STGVLLPLQ	8
6	fx 55 (1566)	(S)QTLQFXE	9	SQTLQFDE	10
	fx 47	VYAF	11	NO MATCH	
	N terminal seq	HAGKYSREKNT(P)A(P)	12	HGGKYSREKNQPKP	13
	fx 57 (1438)	SQTLQFDEQ	14	SQTLQFDEQ	14
	fx 57 (1652)	SLKPSNHA	15	SLKPSNHA	15
7	fx 51 (1093)	AALRPLVKP	16	AALRPLVKP	16
	fx 37 (no MS)	A(H)I(Q)VERYV	17	AIVER	18
	fx 37 (no MS)	A(H)I(Q)VERYV	17	HQSDRYV	19
8	fx 78 ()	XALF(G)AQLGXALGPI	20	NO MATCH	
9	fx 56 (1567)	SQTLQFDEQT	21	SQTLQFDEQT	21

FIG. 15A-1



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Match	Identification	Species	Accession No.	AAs
11/11	Histone H1.c	human	87668 (NCBI)	65-75
11/11	40s Ribosomal Protein S20	rat	R3RT20 (PIR)	31-41
11/14	LORP	mouse	AAC95338 (NCBI)	213-226
15/15	BMP-3	human	4557371 (NCBI)	290-304
20/20	BMP-3	human	4557371 (NCBI)	290-309
9/9	BMP-3	human	4557371 (NCBI)	290-298
7/8	BMP-3	human	4557371 (NCBI)	346-353
	???			
11/14	α 2-MACROGLOBULIN RECEPTOR ASSOC. PRO.	human	P30533 (Swiss-Prot)	31-46
9/9	BMP-3	human	4557371 (NCBI)	346-354
8/8	BMP-3	human	4557371 (NCBI)	410-417
9/9	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	1-9
5/5	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	109-113
5/7	60s Ribosomal Protein L32	mouse	P17932 (Swiss-Prot)	22-28
	???			
10/10	BMP-3	human	P12645 (Swiss-Prot)	346-355

FIG. 15A-2



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Band	Sample	Sequence Data	SEQ. ID NO:	Best Database Match	SEQ. ID NO:
11	fx 55 (1311)	SQTLXF	22	SQTLQF	23
	fx 47 (1772)	VLATVTKPVGGDK	24	VLATVTKPVGGDK	24
	fx 76 (1795)	xVFAL	25	VFAL	25
	fx 61 (1145)	AVPQLQGYLR	26	AIPQLQGYLR	27
18					
22	fx 58 (1101)	ALDAAYCFR	28	ALDAAYCFR	28
	fx 69 (NO MATCH)	GYNANFCAGACPYL	29	GYNANFCAGACPYL	29
	fx 66 (1411.71)	VNSQSLSPY	30	VNSQSLSPY	30
25	fx 39 (1470)	KAAPSV(P)	31	KAAPSV	31
29					

FIG. 15B-1



Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments from 1D Gels

Match	Identification	Species	Accession No.	AAs
5/6	BMP-3	human	4557371 (NCBI)	346-351
13/13	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	87-99
4/4	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	273-276
9/10	60s Ribosomal Protein L6	human	Q02878 (Swiss-Prot)	262-271
9/9	TGF-β2	human	P08112 (Swiss-Prot)	303-311
14/14	TGF-β2	human	P08112 (Swiss-Prot)	340-353
9/9	SPP24	bovine	Q27967 (Swiss-Prot)	42-50
8/8	Histone H1 x	human	JC4928 (PIR)	199-206

FIG. 15B-2



Identifications of Proteins by Mass Spectrometry of Fragments from 2D Gels

SPAL DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAS	% COVERAGE	COMMENTS
				DATA	DATABASE	DIFF			
7	LYS-C 4 PEAKS MATCH WITH TGF- β 2	BOVINE	P21214 (SWISS-PROT)	774.56	774.80	-0.34	26.31	42	
				809.69	809.94	-0.25	32.37		
				1175.12	1175.43	-0.31	88.107		
				3168.10	3166.66	1.44	1-25		
	1 PEAK MATCHES WITH SPP24	BOVINE	Q27957 (SWISS-PROT)	2167.77	2167.51	0.26	42.60	10	
8	TRYPSIN 12 PEAKS MATCH WITH RIBOSOME L3	BOVINE	P38872 (SWISS-PROT)	917.39	917.14	0.25	348.355	37	
				984.23	984.15	0.08	10.18		
				1193.62	1192.40	0.22	286-296		
				1360.67	1360.65	0.02	249-250		
				1484.60	1484.63	0.17	103-114		
				1620.88	1620.82	0.04	103-115		
				1778.64	1777.00	-0.16	34-49		
				2238.43	2238.55	-0.12	30-49		
				2325.99	2325.65	0.34	177-197		
				2681.31	2681.04	0.27	200-223		
				2597.94	2597.43	-0.49	70-98		
				2946.10	2946.35	-0.25	198-223		

FIG. 19B



Identifications of Proteins by Mass Spectrometry of Fragments from 2D Gels

SPAL DIGEST	MASS SPEC PROFILE	SPECIES	ACC. NO.	MS PEAKS			AAS	% COVERAGE	COMMENTS
				DATA	DATABASE	DIFF			
9	TRYPSIN 7 PEAKS MATCH WITH RIBOSOME S3s	MOUSE	P97351 (SWISS- PROT)	920.05	920.10	-0.05	19-25	29	
				1218.29	1218.31	-0.02	152-161		
				1346.62	1346.49	0.13	151-161		
				1516.69	1516.69	0.00	174-166		
				1593.72	1523.82	-0.10	94-106		
				1719.91	1720.00	-0.09	199-212		
				1953.12	1953.16	-0.04	65-81		
10	TRYPSIN 4 PEAKS MATCH WITH RIBOSOME H1.c	HUMAN	87658 (NCBI)	1327.75	1327.68	0.19	34-46	23	
				1579.70	1579.71	-0.01	65-78		
				1707.65	1707.89	-0.24	64-79		
				2147.17	2147.53	-0.36	1-21		
				1168.46	1168.33	0.10	230-239		
11	TRYPSIN 6 PEAKS MATCH WITH RIBOSOME S4	HUMAN	P12750 (SWISS- PROT)	1215.39	1216.39	0.00	134-144	23	
				1354.03	1353.61	0.42	230-241		
				1507.86	1507.88	0.12	198-210		
				1557.75	1557.98	-0.23	37-48		
				2140.34	2140.58	-0.24	221-239		
				2591.60	2591.90	-0.10	77-98		

FIG. 19C